

**10/574084**

## SEQUENCE LISTING

**IAP5 Rec'd PCT/PTO 30 MAR 2006**

&lt;110&gt; ENKAM Pharmaceuticals A/S

&lt;120&gt; A method of modulating cell survival, differentiation and/or synaptic plasticity

&lt;130&gt; P 810 PC00

&lt;160&gt; 45

&lt;170&gt; PatentIn version 3.1

&lt;210&gt; 1

&lt;211&gt; 13

&lt;212&gt; PRT

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; rat NCAM Ig1 fragment: amino acid residues 35-47

&lt;400&gt; 1

Trp	Phe	Ser	Pro	Asn	Gly	Glu	Lys	Leu	Ser	Pro	Asn	Gln
1				5					10			

&lt;210&gt; 2

&lt;211&gt; 14

&lt;212&gt; PRT

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; rat NCAM Ig1 fragment: amino acid residues 75-88

<400> 2

Tyr Lys Cys Val Val Thr Ala Glu Asp Gly Thr Gln Ser Glu  
1 5 10

<210> 3

<211> 12

<212> PRT

<213> Artificial sequence

<220>

<223> rat NCAM Ig3 fragment: amino acid residues 213-224

<400> 3

Thr Leu Val Ala Asp Ala Asp Gly Phe Pro Glu Pro  
1 5 10

<210> 4

<211> 9

<212> PRT

<213> Artificial sequence

<220>

<223> rat NCAM Ig2 fragment: amino acid residues 156-164

<400> 4

Gln Ile Arg Gly Ile Lys Lys Thr Asp  
1 5

<210> 5

<211> 3

<212> PRT

<213> Artificial sequence

<220>

<223> rat NCAM Ig2 fragment: amino acid residues 144-146

<400> 5

Asp Val Arg  
1

<210> 6

<211> 7

<212> PRT

<213> Artificial sequence

<220>

<223> rat NCAM Ig2 fragment: amino acid residues 158-164

<400> 6

Arg Gly Ile Lys Lys Thr Asp  
1 5

<210> 7

<211> 10

<212> PRT

<213> Artificial sequence

<220>

<223> rat NCAM Ig2 fragment: amino acid residues 144-146 and 158-164

<400> 7

Asp Val Arg Arg Gly Ile Lys Lys Thr Asp  
1 5 10

<210> 8

<211> 5

<212> PRT

<213> Artificial sequence

<220>

<223> rat NCAM Ig2 fragment: amino acid residues 111-115

<400> 8

Lys Glu Gly Glu Asp  
1 5

<210> 9

<211> 8

<212> PRT

<213> Artificial sequence

<220>

<223> rat NCAM Ig2 fragment: amino acid residues 157-164

<400> 9

Ile Arg Gly Ile Lys Lys Thr Asp  
1 5

<210> 10

<211> 14

<212> PRT

<213> Artificial sequence

<220>

<223> rat NCAM Ig2 fragment: amino acid residues 111-115 and 157-164

<400> 10

Lys Glu Gly Glu Asp Gly Ile Arg Gly Ile Lys Lys Thr Asp  
1 5 10

<210> 11

<211> 5

<212> PRT

<213> Artificial sequence

<220>

<223> rat NCAM Ig3 fragment: amino acid residues 260-264

<400> 11

Asp Lys Asn Asp Glu  
1 5

<210> 12

<211> 12

<212> PRT

<213> Artificial sequence

<220>

<223> rat NCAM Ig3 fragment: amino acid residues 194-205

<400> 12

Thr Val Gln Ala Arg Asn Ser Ile Val Asn Ala Thr  
1 5 10

<210> 13

<211> 9

<212> PRT

<213> Artificial sequence

<220>

<223> rat NCAM Ig3 fragment: amino acid residues 281-289

<400> 13

Ser Ile His Leu Lys Val Phe Ala Lys  
1 5

<210> 14

<211> 9

<212> PRT

<213> Artificial sequence

<220>

<223> rat NCAM Ig2 fragment: amino acid residues 150-158

<400> 14

Leu Ser Asn Asn Tyr Leu Gln Ile Arg  
1 5

<210> 15

<211> 12

<212> PRT

<213> Artificial sequence

<220>

<223> rat NCAM Ig2 fragment: amino acid residues 146-157

<400> 15

Arg Phe Ile Val Leu Ser Asn Asn Tyr Leu Gln Ile  
1 5 10

<210> 16

<211> 16

<212> PRT

<213> Artificial sequence

<220>

<223> rat NCAM Ig2 fragment: amino acid residues 142-157

<400> 16

Lys Lys Asp Val Arg Phe Ile Val Leu Ser Asn Asn Tyr Leu Gln Ile  
1 5 10 15

<210> 17

<211> 12

<212> PRT

<213> Artificial sequence

&lt;220&gt;

&lt;223&gt; rat NCAM Ig2 fragment: amino acid residues 108-119

&lt;400&gt; 17

Gln	Glu	Phe	Lys	Glu	Gly	Glu	Asp	Ala	Val	Ile	Val
1				5					10		

&lt;210&gt; 18

&lt;211&gt; 11

&lt;212&gt; PRT

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; rat NCAM Ig2 fragment: amino acid residues 111-121

&lt;400&gt; 18

Lys	Glu	Gly	Glu	Asp	Ala	Val	Ile	Val	Cys	Asp
1				5					10	

&lt;210&gt; 19

&lt;211&gt; 12

&lt;212&gt; PRT

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; rat NCAM Ig1 fragment: amino acid residues 10-21

&lt;400&gt; 19

Gly	Glu	Ile	Ser	Val	Gly	Glu	Ser	Lys	Phe	Phe	Leu
1				5					10		

&lt;210&gt; 20

&lt;211&gt; 21

&lt;212&gt; PRT

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; rat NCAM Ig3 fragment: amino acid residues 243-263

&lt;400&gt; 20

Lys His Ile Phe Ser Asp Asp Ser Ser Glu Leu Thr Ile Arg Asn Val  
1 5 10 15

Asp Lys Asn Asp Glu  
20

&lt;210&gt; 21

&lt;211&gt; 12

&lt;212&gt; PRT

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; rat NCAM Ig1 fragment : amino acid residues 10-21 containing mutation F19A

&lt;400&gt; 21

Gly Glu Ile Ser Val Gly Glu Ser Lys Ala Phe Leu  
1 5 10

&lt;210&gt; 22

&lt;211&gt; 12

&lt;212&gt; PRT

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; rat NCAN Ig1 fragment: amino acid residues 10-21 containing mutations F19A and F20A

&lt;400&gt; 22

Gly Glu Ile Ser Val Gly Glu Ser Lys Ala Ala Leu  
1 5 10



<210> 23

<211> 21

<212> PRT

<213> Artificial sequence

<220>

<223> chicken NCAM Ig3 fragment: amino acid residues 243-263

<400> 23

Lys Tyr Ser Phe Asn Tyr Asp Gly Ser Glu Leu Ile Ile Lys Lys Val  
1 5 10 15

Asp Lys Ser Asp Glu  
20

<210> 24

<211> 10

<212> PRT

<213> Artificial sequence

<220>

<223> rat NCAM Ig3 fragment: amino acid residues 244-253

<400> 24

Lys His Ile Phe Ser Asp Asp Ser Ser Glu  
1 5 10

<210> 25

<211> 10

<212> PRT

<213> Artificial sequence

<220>

<223> chicken NCAM Ig3 fragment: amino acid residues 243-252

<400> 25

Lys Tyr Ser Phe Asn Tyr Asp Gly Ser Glu  
1                      5                      10

<210> 26

<211> 9

<212> PRT

<213> Artificial sequence

<220>

<223> rat NCAM Ig3 fragment: amino acid residues 281-289 containing mutations K285A and F287S

<400> 26

Ser Ile His Leu Ala Val Ala Ala Lys  
1                      5

<210> 27

<211> 9

<212> PRT

<213> Artificial sequence

<220>

<223> rat NCAM Ig3 fragment: amino acid residues 281-289 containing mutations K285A and F287G

<400> 27

Ser Ile His Leu Ala Val Gly Ala Lys  
1                      5

<210> 28

<211> 12

<212> PRT

<213> Artificial sequence

<220>

<223> rat NCAM Ig2 fragment: amino acid residues 172-182

<400> 28

Gly Arg Ile Leu Ala Arg Gly Glu Ile Asn Phe Lys  
1                      5                      10

<210> 29

<211> 29

<212> DNA

<213> Artificial sequence

<220>

<223> upper PCR primer

<400> 29

tctctcgaga actgcaggta gatattggt

29

<210> 30

<211> 27

<212> DNA

<213> Artificial sequence

<220>

<223> lower PCR primer

<400> 30

aaacccgggt tactttgcaa agacctt

27

<210> 31

<211> 25

<212> DNA

<213> Artificial sequence

<220>

<223> upper PCR primer

<400> 31

gaatacgtaa ctgtccaggc cagac

<210> 32

<211> 27

<212> DNA

<213> Artificial sequence

<220>

<223> lower PCR primer

<400> 32

aaacctagggt tactttgcaa agacctt

27

<210> 33

<211> 75

<212> DNA

<213> Artificial sequence

<220>

<223> upper PCR primer

<400> 33

ctgcaggtag atattgttcc cagccaagga gccatcagcg ttggagcctc cgccttcttc

60

ctgtgtcaag tggca

75

<210> 34

<211> 36

<212> DNA

<213> Artificial sequence

<220>

<223> upper PCR primer

<400> 34

ggcgacagtt cggcgtaac catcaggaat gtggac

36

<210> 35

<211> 39

<212> DNA

<213> Artificial sequence

<220>

<223> lower PCR primer

<400> 35

ggttaacgcc gaactgtcgc cactgaagat gtgcttctc

39

<210> 36

<211> 45

<212> DNA

<213> Artificial sequence

<220>

<223> lower PCR primer

<400> 36

aaacttaggt tactttgctg cgactgcgag gtggatggag gcatc

45

<210> 37

<211> 29

<212> DNA

<213> Artificial sequence

<220>

<223> PCR primer

<400> 37

tctctcgagt tctgcaggta gatattgtt

29

<210> 38

<211> 36

<212> DNA

<213> Artificial sequence

<220>

<223> PCR primer

<400> 38

aaatacgtaa ctgtccaggc cgcccagagc atcgtg

36

<210> 39

<211> 16

<212> PRT

<213> Artificial sequence

<220>

<223> rat NCAM Ig2 fragment: amino acid residues 133-148

<400> 39

Lys His Lys Gly Arg Asp Val Ile Leu Lys Lys Asp Val Arg Phe Ile  
1 5 10 15

<210> 40

<211> 13

<212> PRT

<213> Artificial sequence

<220>

<223> NCAM Ig1 fargment: CD-srands

<400> 40

Ala Phe Ser Pro Asn Gly Glu Lys Leu Ser Pro Asn Gln  
1 5 10

<210> 41

<211> 14

<212> PRT

<213> Artificial sequence

<220>

<223> NCAM Ig1 fragment: FG-strands

<400> 41

Ala	Lys	Ser	Val	Val	Thr	Ala	Glu	Asp	Gly	Thr	Gln	Ser	Glu
1				5					10				

<210> 42

<211> 10

<212> PRT

<213> Artificial sequence

<220>

<223> NCAM Ig2 fragment: CD-strands

<400> 42

Asp	Val	Arg	Arg	Gly	Ile	Lys	Lys	Thr	Asp
1				5					10

<210> 43

<211> 9

<212> PRT

<213> Artificial sequence

<220>

<223> NCAM Ig2 fragment: EF-strands

<400> 43

Gln	Ile	Arg	Gly	Ile	Lys	Lys	Thr	Asp
1				5				

<210> 44

<211> 858

<212> PRT

&lt;213&gt; Rattus norvegicus

&lt;400&gt; 44

Met Leu Arg Thr Lys Asp Leu Ile Trp Thr Leu Phe Phe Leu Gly Thr  
 1 5 10 15

Ala Val Ser Leu Gln Val Asp Ile Val Pro Ser Gln Gly Glu Ile Ser  
 20 25 30

Val Gly Glu Ser Lys Phe Phe Leu Cys Gln Val Ala Gly Asp Ala Lys  
 35 40 45

Asp Lys Asp Ile Ser Trp Phe Ser Pro Asn Gly Glu Lys Leu Ser Pro  
 50 55 60

Asn Gln Gln Arg Ile Ser Val Val Trp Asn Asp Asp Asp Ser Ser Thr  
 65 70 75 80

Leu Thr Ile Tyr Asn Ala Asn Ile Asp Asp Ala Gly Ile Tyr Lys Cys  
 85 90 95

Val Val Thr Ala Glu Asp Gly Thr Gln Ser Glu Ala Thr Val Asn Val  
 100 105 110

Lys Ile Phe Gln Lys Leu Met Phe Lys Asn Ala Pro Thr Pro Gln Glu  
 115 120 125

Phe Lys Glu Gly Glu Asp Ala Val Ile Val Cys Asp Val Val Ser Ser  
 130 135 140

Leu Pro Pro Thr Ile Ile Trp Lys His Lys Gly Arg Asp Val Ile Leu  
 145 150 155 160

Lys Lys Asp Val Arg Phe Ile Val Leu Ser Asn Asn Tyr Leu Gln Ile  
 165 170 175

Arg Gly Ile Lys Lys Thr Asp Glu Gly Thr Tyr Arg Cys Glu Gly Arg  
 180 185 190

Ile Leu Ala Arg Gly Glu Ile Asn Phe Lys Asp Ile Gln Val Ile Val  
 195 200 205



Asn	Val	Pro	Pro	Thr	Val	Gln	Ala	Arg	Gln	Ser	Ile	Val	Asn	Ala	Thr	210	215	220	
Ala	Asn	Leu	Gly	Gln	Ser	Val	Thr	Leu	Val	Cys	Asp	Ala	Asp	Gly	Phe	225	230	235	240
Pro	Glu	Pro	Thr	Met	Ser	Trp	Thr	Lys	Asp	Gly	Glu	Pro	Ile	Glu	Asn	245	250	255	
Glu	Glu	Glu	Asp	Asp	Glu	Lys	His	Ile	Phe	Ser	Asp	Asp	Ser	Ser	Glu	260	265	270	
Leu	Thr	Ile	Arg	Asn	Val	Asp	Lys	Asn	Asp	Glu	Ala	Glu	Tyr	Val	Cys	275	280	285	
Ile	Ala	Glu	Asn	Lys	Ala	Gly	Glu	Gln	Asp	Ala	Ser	Ile	His	Leu	Lys	290	295	300	
Val	Phe	Ala	Lys	Pro	Lys	Ile	Thr	Tyr	Val	Glu	Asn	Gln	Thr	Ala	Met	305	310	315	320
Glu	Leu	Glu	Glu	Gln	Val	Thr	Leu	Thr	Cys	Glu	Ala	Ser	Gly	Asp	Pro	325	330	335	
Ile	Pro	Ser	Ile	Thr	Trp	Arg	Thr	Ser	Thr	Arg	Asn	Ile	Ser	Ser	Glu	340	345	350	
Glu	Lys	Ala	Ser	Trp	Thr	Arg	Pro	Glu	Lys	Gln	Glu	Thr	Leu	Asp	Gly	355	360	365	
His	Met	Val	Val	Arg	Ser	His	Ala	Arg	Val	Ser	Ser	Leu	Thr	Leu	Lys	370	375	380	
Ser	Ile	Gln	Tyr	Thr	Asp	Ala	Gly	Glu	Tyr	Ile	Cys	Thr	Ala	Ser	Asn	385	390	395	400
Thr	Ile	Gly	Gln	Asp	Ser	Gln	Ser	Met	Tyr	Leu	Glu	Val	Gln	Tyr	Ala	405	410	415	
Pro	Lys	Leu	Gln	Gly	Pro	Val	Ala	Val	Tyr	Thr	Trp	Glu	Gly	Asn	Gln	420	425	430	
Val	Asn	Ile	Thr	Cys	Glu	Val	Phe	Ala	Tyr	Pro	Ser	Ala	Thr	Ile	Ser	435	440	445	

Trp Phe Arg Asp Gly Gln Leu Leu Pro Ser Ser Asn Tyr Ser Asn Ile  
 450 455 460

Lys Ile Tyr Asn Thr Pro Ser Ala Ser Tyr Leu Glu Val Thr Pro Asp  
 465 470 475 480

Ser Glu Asn Asp Phe Gly Asn Tyr Asn Cys Thr Ala Val Asn Arg Ile  
 485 490 495

Gly Gln Glu Ser Leu Glu Phe Ile Leu Val Gln Ala Asp Thr Pro Ser  
 500 505 510

Ser Pro Ser Ile Asp Arg Val Glu Pro Tyr Ser Ser Thr Ala Gln Val  
 515 520 525

Gln Phe Asp Glu Pro Glu Ala Thr Gly Gly Val Pro Ile Leu Lys Tyr  
 530 535 540

Lys Ala Glu Trp Lys Ser Leu Gly Glu Glu Ala Trp His Ser Lys Trp  
 545 550 555 560

Tyr Asp Ala Lys Glu Ala Asn Met Glu Gly Ile Val Thr Ile Met Gly  
 565 570 575

Leu Lys Pro Glu Thr Arg Tyr Ala Val Arg Leu Ala Ala Leu Asn Gly  
 580 585 590

Lys Gly Leu Gly Glu Ile Ser Ala Ala Thr Glu Phe Lys Thr Gln Pro  
 595 600 605

Val Arg Glu Pro Ser Ala Pro Lys Leu Glu Gly Gln Met Gly Glu Asp  
 610 615 620

Gly Asn Ser Ile Lys Val Asn Leu Ile Lys Gln Asp Asp Gly Gly Ser  
 625 630 635 640

Pro Ile Arg His Tyr Leu Val Lys Tyr Arg Ala Leu Ala Ser Glu Trp  
 645 650 655

Lys Pro Glu Ile Arg Leu Pro Ser Gly Ser Asp His Val Met Leu Lys  
 660 665 670

Ser Leu Asp Trp Asn Ala Glu Tyr Glu Val Tyr Val Val Ala Glu Asn  
 675 680 685

Gln Gln Gly Lys Ser Lys Ala Ala His Phe Val Phe Arg Thr Ser Ala  
 690 695 700

Gln Pro Thr Ala Ile Pro Ala Asn Gly Ser Pro Thr Ala Gly Leu Ser  
 705 710 715 720

Thr Gly Ala Ile Val Gly Ile Leu Ile Val Ile Phe Val Leu Leu Leu  
 725 730 735

Val Val Met Asp Ile Thr Cys Tyr Phe Leu Asn Lys Cys Gly Leu Leu  
 740 745 750

Met Cys Ile Ala Val Asn Leu Cys Gly Lys Ala Gly Pro Gly Ala Lys  
 755 760 765

Gly Lys Asp Met Glu Glu Gly Lys Ala Ala Phe Ser Lys Asp Glu Ser  
 770 775 780

Lys Glu Pro Ile Val Glu Val Arg Thr Glu Glu Glu Arg Thr Pro Asn  
 785 790 795 800

His Asp Gly Gly Lys His Thr Glu Pro Asn Glu Thr Thr Pro Leu Thr  
 805 810 815

Glu Pro Glu Lys Gly Pro Val Glu Thr Lys Ser Glu Pro Gln Glu Ser  
 820 825 830

Glu Ala Lys Pro Ala Pro Thr Glu Val Lys Thr Val Pro Asn Glu Ala  
 835 840 845

Thr Gln Thr Lys Glu Asn Glu Ser Lys Ala  
 850 855

<210> 45

<211> 848

<212> PRT

<213> Homo sapiens

<400> 45

Met Leu Gln Thr Lys Asp Leu Ile Trp Thr Leu Phe Phe Leu Gly Thr

1	5	10	15
Ala Val Ser	Leu Gln Val Asp Ile Val	Pro Ser Gln Gly Glu Ile Ser	
	20	25	30
Val Gly Glu Ser Lys Phe Phe	Leu Cys Gln Val Ala Gly Asp Ala Lys		
	35	40	45
Asp Lys Asp Ile Ser Trp Phe Ser Pro Asn Gly Glu Lys Leu Thr Pro			
50	55	60	
Asn Gln Gln Arg Ile Ser Val Val Trp Asn Asp Asp Ser Ser Ser Thr			
65	70	75	80
Leu Thr Ile Tyr Asn Ala Asn Ile Asp Asp Ala Gly Ile Tyr Lys Cys			
	85	90	95
Val Val Thr Gly Glu Asp Gly Ser Glu Ser Glu Ala Thr Val Asn Val			
	100	105	110
Lys Ile Phe Gln Lys Leu Met Phe Lys Asn Ala Pro Thr Pro Gln Glu			
	115	120	125
Phe Arg Glu Gly Glu Asp Ala Val Ile Val Cys Asp Val Val Ser Ser			
	130	135	140
Leu Pro Pro Thr Ile Ile Trp Lys His Lys Gly Arg Asp Val Ile Leu			
145	150	155	160
Lys Lys Asp Val Arg Phe Ile Val Leu Ser Asn Asn Tyr Leu Gln Ile			
	165	170	175
Arg Gly Ile Lys Lys Thr Asp Glu Gly Thr Tyr Arg Cys Glu Gly Arg			
	180	185	190
Ile Leu Ala Arg Gly Glu Ile Asn Phe Lys Asp Ile Gln Val Ile Val			
	195	200	205
Asn Val Pro Pro Thr Ile Gln Ala Arg Gln Asn Ile Val Asn Ala Thr			
	210	215	220
Ala Asn Leu Gly Gln Ser Val Thr Leu Val Cys Asp Ala Glu Gly Phe			
225	230	235	240

Pro Glu Pro Thr Met Ser Trp Thr Lys Asp Gly Glu Gln Ile Glu Gln  
 245 250 255

Glu Glu Asp Asp Glu Lys Tyr Ile Phe Ser Asp Asp Ser Ser Gln Leu  
 260 265 270

Thr Ile Lys Lys Val Asp Lys Asn Asp Glu Ala Glu Tyr Ile Cys Ile  
 275 280 285

Ala Glu Asn Lys Ala Gly Glu Gln Asp Ala Thr Ile His Leu Lys Val  
 290 295 300

Phe Ala Lys Pro Lys Ile Thr Tyr Val Glu Asn Gln Thr Ala Met Glu  
 305 310 315 320

Leu Glu Glu Gln Val Thr Leu Thr Cys Glu Ala Ser Gly Asp Pro Ile  
 325 330 335

Pro Ser Ile Thr Trp Arg Thr Ser Thr Arg Asn Ile Ser Ser Glu Glu  
 340 345 350

Lys Thr Leu Asp Gly His Met Val Val Arg Ser His Ala Arg Val Ser  
 355 360 365

Ser Leu Thr Leu Lys Ser Ile Gln Tyr Thr Asp Ala Gly Glu Tyr Ile  
 370 375 380

Cys Thr Ala Ser Asn Thr Ile Gly Gln Asp Ser Gln Ser Met Tyr Leu  
 385 390 395 400

Glu Val Gln Tyr Ala Pro Lys Leu Gln Gly Pro Val Ala Val Tyr Thr  
 405 410 415

Trp Glu Gly Asn Gln Val Asn Ile Thr Cys Glu Val Phe Ala Tyr Pro  
 420 425 430

Ser Ala Thr Ile Ser Trp Phe Arg Asp Gly Gln Leu Leu Pro Ser Ser  
 435 440 445

Asn Tyr Ser Asn Ile Lys Ile Tyr Asn Thr Pro Ser Ala Ser Tyr Leu  
 450 455 460

Glu Val Thr Pro Asp Ser Glu Asn Asp Phe Gly Asn Tyr Asn Cys Thr  
 465 470 475 480

Ala Val Asn Arg Ile Gly Gln Glu Ser Leu Glu Phe Ile Leu Val Gln  
                   485                                  490                                  495

Ala Asp Thr Pro Ser Ser Pro Ser Ile Asp Gln Val Glu Pro Tyr Ser  
                   500                                  505                                  510

Ser Thr Ala Gln Val Gln Phe Asp Glu Pro Glu Ala Thr Gly Gly Val  
                   515                                  520                                  525

Pro Ile Leu Lys Tyr Lys Ala Glu Trp Arg Ala Val Gly Glu Glu Val  
                   530                                  535                                  540

Trp His Ser Lys Trp Tyr Asp Ala Lys Glu Ala Ser Met Glu Gly Ile  
                   545                                  550                                  555                                  560

Val Thr Ile Val Gly Leu Lys Pro Glu Thr Thr Tyr Ala Val Arg Leu  
                   565                                  570                                  575

Ala Ala Leu Asn Gly Lys Gly Leu Gly Glu Ile Ser Ala Ala Ser Glu  
                   580                                  585                                  590

Phe Lys Thr Gln Pro Val Gln Gly Glu Pro Ser Ala Pro Lys Leu Glu  
                   595                                  600                                  605

Gly Gln Met Gly Glu Asp Gly Asn Ser Ile Lys Val Asn Leu Ile Lys  
                   610                                  615                                  620

Gln Asp Asp Gly Gly Ser Pro Ile Arg His Tyr Leu Val Arg Tyr Arg  
                   625                                  630                                  635                                  640

Ala Leu Ser Ser Glu Trp Lys Pro Glu Ile Arg Leu Pro Ser Gly Ser  
                   645                                  650                                  655

Asp His Val Met Leu Lys Ser Leu Asp Trp Asn Ala Glu Tyr Glu Val  
                   660                                  665                                  670

Tyr Val Val Ala Glu Asn Gln Gln Gly Lys Ser Lys Ala Ala His Phe  
                   675                                  680                                  685

Val Phe Arg Thr Ser Ala Gln Pro Thr Ala Ile Pro Ala Asn Gly Ser  
                   690                                  695                                  700

Pro Thr Ser Gly Leu Ser Thr Gly Ala Ile Val Gly Ile Leu Ile Val  
                   705                                  710                                  715                                  720

Ile Phe Val Leu Leu Leu Val Val Val Asp Ile Thr Cys Tyr Phe Leu  
725 730 735

Asn Lys Cys Gly Leu Phe Met Cys Ile Ala Val Asn Leu Cys Gly Lys  
740 745 750

Ala Gly Pro Gly Ala Lys Gly Lys Asp Met Glu Glu Gly Lys Ala Ala  
755 760 765

Phe Ser Lys Asp Glu Ser Lys Glu Pro Ile Val Glu Val Arg Thr Glu  
770 775 780

Glu Glu Arg Thr Pro Asn His Asp Gly Gly Lys His Thr Glu Pro Asn  
785 790 795 800

Glu Thr Thr Pro Leu Thr Glu Pro Glu Lys Gly Pro Val Glu Ala Lys  
805 810 815

Pro Glu Cys Gln Glu Thr Glu Thr Lys Pro Ala Pro Ala Glu Val Lys  
820 825 830

Thr Val Pro Asn Asp Ala Thr Gln Thr Lys Glu Asn Glu Ser Lys Ala  
835 840 845